SEQUENCE LISTING

```
<110> Allen, Keith D.
      Matthews, William
      Moore, Mark
```

<120> TRANSGENIC MICE CONTAINING ADRENOCORTICOTROPIN HORMONE RECEPTOR GENE DISRUPTIONS

```
<130> R-605
<140> To Be Assigned
<141> Herewith
<150> US 60/254,906
<151> 2000-12-11
<150> US 60/324,583
<151> 2001-09-24
<160> 4
<170> FastSEQ for Windows Version 4.0
<210> 1
<211> 1100
<212> DNA
<213> Mus musculus
<400> 1
atttatttat ttaatcatct catatgtgtc tatgtgttct gtttaacctc agatccttcc 60
acacaaagaa aacatactgc agaaacaatc gtgatttctg taagtcaacg gcaaacacca 120
cccccgtctt aacggccagc aggaaaaaat gaagcatatt atcaattcgt atgaacacac 180
caatgacacc gcaagaaata actccgattg tcctgatgta gttttgccag aagagatatt 240
tttcacaatc tctgtcattg gcatattgga gaacttgatt gtcctcctgg ctgtgatcaa 300
aaataaaaat ctccagtccc ccatgtattt tttcatctgc agtttggcca tttctgacat 360
gttgggcagt ctgtataaga tcttggaaaa catcctgatc atgttcagaa acatgggtta 420
tettaageet egtggeagtt ttgaaageae ageagatgae ateattgaet geatgtteat 480
cetetetttg etgggeteta tetteageet gtetgteatt geagetgaee gttacateae 540
catcttccat gccctgcaat accatagcat tgtgaccatg cgccgcacca tcatcaccct 600
aacaattatc tggatgttct gcacagggag cggcatcacc atggtgatct tctcccacca 660
catccccaca gtgctcacct tcacatcgct gttccctttg atgctggttt ttatcctgtg 720
tetetacate caeatgttet taettgeeeg eteceatget aggaagatet etaceettee 780
tagaaccaac atgaagggtg ccatgacact aaccatcctt cttggagtct tcatcttctg 840
ttgggccccc tttgtgctcc atgttctctt aatgaccttc tgcccaaata acccttactg 900
tgtttgctac atgtctctct tccaggtcaa tggcatgttg atcatgtgca atgcagttat 960
tgaccccttt atatatgcct ttcggagccc agagctcaga gatgcattca aaaggatgct 1020
cttctgcaac cggtattagt agaatttttg atccctgctt tgagtgttgt aaagggacca 1080
aataacacat cagtctgaca
<210> 2
<211> 296
```

<212> PRT

<213> Mus musculus

<400> 2

Met Lys His Ile Ile Asn Ser Tyr Glu His Thr Asn Asp Thr Ala Arg 5 10 Asn Asn Ser Asp Cys Pro Asp Val Val Leu Pro Glu Glu Ile Phe Phe

<223> Targeting Vector

<400> 4

```
25
            20
Thr Ile Ser Val Ile Gly Ile Leu Glu Asn Leu Ile Val Leu Leu Ala
                                                 45
                            40
Val Ile Lys Asn Lys Asn Leu Gln Ser Pro Met Tyr Phe Phe Ile Cys
Ser Leu Ala Ile Ser Asp Met Leu Gly Ser Leu Tyr Lys Ile Leu Glu
                    70
Asn Ile Leu Ile Met Phe Arg Asn Met Gly Tyr Leu Lys Pro Arg Gly
                                     90
Ser Phe Glu Ser Thr Ala Asp Asp Ile Ile Asp Cys Met Phe Ile Leu
                                105
                                                      110
            100
Ser Leu Leu Gly Ser Ile Phe Ser Leu Ser Val Ile Ala Ala Asp Arg
                             120
                                                 125
Tyr Ile Thr Ile Phe His Ala Leu Gln Tyr His Ser Ile Val Thr Met
                                             140
                        135
Arg Arg Thr Ile Ile Thr Leu Thr Ile Ile Trp Met Phe Cys Thr Gly
                                                              160
                                         155
                    150
Ser Gly Ile Thr Met Val Ile Phe Ser His His Ile Pro Thr Val Leu
                                                          175
                165
                                     170
Thr Phe Thr Ser Leu Phe Pro Leu Met Leu Val Phe Ile Leu Cys Leu
                                 185
            180
Tyr Ile His Met Phe Leu Leu Ala Arg Ser His Ala Arg Lys Ile Ser
                                                 205
                             200
        195
Thr Leu Pro Arg Thr Asn Met Lys Gly Ala Met Thr Leu Thr Ile Leu
                                             220
                         215
Leu Gly Val Phe Ile Phe Cys Trp Ala Pro Phe Val Leu His Val Leu
                                         235
                     230
Leu Met Thr Phe Cys Pro Asn Asn Pro Tyr Cys Val Cys Tyr Met Ser
                                     250
                245
Leu Phe Gln Val Asn Gly Met Leu Ile Met Cys Asn Ala Val Ile Asp
                                 265
            260
Pro Phe Ile Tyr Ala Phe Arg Ser Pro Glu Leu Arg Asp Ala Phe Lys
                             280
                                                  285
        275
Arg Met Leu Phe Cys Asn Arg Tyr
    290
<210> 3
<211> 200
<212> DNA
<213> Artificial Sequence
<220>
<223> Targeting Vector
<400> 3
atgaacacac caatgacacc gcaagaaata actccgattg tcctgatgta gttttgccag 60
aagagatatt tttcacaatc tctgtcattg gcatattgga gaacttgatt gtcctcctgg 120
ctgtgatcaa aaataaaaat ctccagtccc ccatgtattt tttcatctgc agtttggcca 180
                                                                    200
tttctgacat gttgggcagt
<210> 4
<211> 200
<212> DNA
<213> Artificial Sequence
<220>
```

ggtgccatga cactaaccat ccttcttgga gtcttcatct tctgttgggc cccctttgtg 60

ctccatgttc tcttaatgac tttctgccca aataaccctt actgtgtttg ctacatgtct 120 ctcttccagg tcaatggcat gttgatcatg tgcaatgcag ttattgaccc ctttatatat 180 gcctttcgga gcccagagct 200